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A new species of *Goniurosaurus* (Sauria, Gekkota, Eublepharidae) from Guangxi, China

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Abstract

In recent years, with advances in field surveys and molecular biology research, many new species of *Goniurosaurus* have been discovered, enhancing our understanding of their diversity and distribution. In this study, we present an integrated analysis of morphological evidence and mitochondrial and nuclear DNA sequence data to describe a new species from Guilin, Guangxi Zhuang Autonomous Region, China: *Goniurosaurus wuzhengjuni* **sp. nov.** This species can be distinguished morphologically from its congeners by a specific combination of characteristics: (1) 23 precloacal pores in males; (2) a grayish-white dorsal ground color on the head, body, and limbs covered with dense, irregular black blotches; (3) seven nasal scales surrounding the nostril; and (4) 101–108 midbody scale rows. Phylogenetic analyses indicate that this species forms a monophyletic lineage sister to *G. araneus* within the *G. luii* group, as supported by mitochondrial cyt *b* and 16S rRNA and nuclear *C-mos* gene sequences. Uncorrected pairwise genetic distances based on mitochondrial cyt *b* sequences range from 8.7% to 22.0% compared with those of all previously known species.

Key Words

Goniurosaurus wuzhengjuni sp. nov., molecular phylogeny, morphology, taxonomy

Introduction

The genus *Goniurosaurus* Barbour, 1908, known as cave geckos, includes 25 recognized species distributed across Guangxi, Guizhou, Guangdong, and Hainan in China, as well as in Vietnam and Japan's Ryukyu Islands (Grismer et al. 2021; Ngo et al. 2021; Cai et al. 2022; Kurita and Toda 2024; Qi et al. 2025). Phylogenetic analyses have classified the genus into four well-supported species groups: the *G. kuroiwae* group (*G. nebulozonatus*, *G. sengokui*, *G. yamashinae*, *G. kuroiwae*, *G. orientalis* and *G. toyamai*), the *G. lichtenfelderi* group (*G. lichtenfelderi*, *G. hainanensis*, *G. zhoui* and *G. bawanglingensis*), the *G. luii* group (*G. liboensis*, *G. kwangsiensis*, *G. luii*, *G. huuliensis*, *G. araneus*, *G. gezhi*, *G. chengzheng* and *G. catbaensis*), and the *G. yingdeensis* group (*G. gollum*, *G. wangshu*, *G. yingdeensis*, *G. varius* and *G. zhelongi*) (Liang et al. 2018; Zhu et al. 2020a, 2022; Grismer et al. 2021; Kurita and Toda 2024; Qi et al. 2025). Species of *Goniurosaurus* typically inhabit karst landscapes, tropical rainforests, and seasonal monsoon forests, where they inhabit terrestrial microhabitats such as forest floors, limestone crevices, and caves—often in proximity to riparian zones (Grismer et al. 1999; Wang et al. 2010; Wang et al. 2013; Yang and Chan 2015). As nocturnal rock-dwelling reptiles, they predominantly feed on a diverse array of small invertebrate prey (Grismer et al. 2021).

During field surveys conducted in 2025 in the northern region of the Guangxi Zhuang Autonomous Region, China, several specimens exhibiting morphological characteristics consistent with members of *Goniurosaurus*

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were collected from the Baishou Nature Reserve, Yongfu County, Guilin City, Guangxi. Subsequent integrative analyses combining morphological and molecular data revealed that these specimens represent a distinct taxonomic lineage. Although it is assignable to the *G. luii* group, this lineage differs markedly from all known congeners. The comprehensive evidence supports the recognition of this population as a new, previously undescribed species within the genus *Goniurosaurus*. The discovery of this new species not only enriches our understanding of *Goniurosaurus* diversity in southern China but also underscores the importance of continued biodiversity surveys in karst ecosystems.

Materials and methods

Sampling

During herpetofaunal surveys conducted in the Baishou Nature Reserve, four specimens of *Goniurosaurus* (voucher numbers GXNU2025090812 and GXNU2025101601–03) were collected. All specimens were fixed and preserved in 75% ethanol, and partial muscle tissues were sampled and stored at –80 °C in an ultra-low-temperature freezer for subsequent molecular analyses. All voucher specimens are deposited in the Herpetological Collection of Guangxi Normal University (GXNU), Guilin, China.

Morphology

Morphometric measurements followed the protocol of Ziegler et al. (2008), using a vernier caliper (DL3945, 0–200 mm range, 0.03 mm accuracy; Deli Tools Co., Ningbo, China). The following measurements were recorded: snout–vent length (**SVL**; tip of snout to vent); tail length (**TaL**; vent to tip of tail); distance between axilla and groin (**AG**; from posterior edge of forelimb insertion to anterior edge of hindlimb insertion); snout–eye distance (**SE**; from tip of snout to anteriormost margin of eye); eye–ear distance (**EE**; from posterior margin of eye to posterior margin of ear); head width (**HW**; maximum width) and head length (**HL**; from tip of snout to posterior margin of ear).

The following scalation characters were counted: supralabials (**SPL**); sublabials (**SBL**); nasal scales surrounding nare (**SN**); internasals (**IN**); gular scales bordering the internasals (**PostIN**); postmentals (**PM**); gular scales bordering the postmentals (**GP**); eyelid fringe scales or ciliaria (**CIL**); granular scales surrounding dorsal tubercles (**GST**); dorsal tubercle rows at midbody (**DTR**); paravertebral tubercles between limb insertions (**TL**); scales around midbody (**MB**); subdigital lamellae under the first (**LD1**) and fourth fingers (**LD4**); subdigital lamellae under the first (**LT1**) and fourth toes (**LT4**); precloacal pores (**PP**); and postcloacal tubercles (**PAT**). Bilateral characters are expressed as left/right.

Phylogenetic analyses

Genomic DNA was extracted from muscle tissue using an Animal Tissue DNA Extraction Kit (Tiangen Biochemical Technology Co., Ltd., Beijing, China) following the manufacturer's protocol. Three loci were amplified and sequenced, including two mitochondrial genes—the cytochrome b (cyt *b*) gene using primers Cyt *b*-2019F/Cyt *b*-2019R (Zhu et al. 2020b) and the 16S ribosomal RNA (16S rRNA) gene using primers r16S-5L/16sbr-H (Jonniaux and Kumazawa 2008)—and one nuclear gene, the oocyte maturation factor (*C*-mos) gene, using primers FU-F/FU-R (Gamble et al. 2008). A total of 139 sequences from 24 species of *Goniurosaurus* were retrieved from GenBank and GenBase, with *Holodactylus africanus* Boettger, 1893 and *Gekko chinensis* Gray, 1842 designated as outgroups, as in Zhu et al. (2021) (Suppl. material 1).

Multiple sequence alignment was conducted using the MUSCLE algorithm implemented in MEGA X (Kumar et al. 2018). Pairwise genetic distances (*p*-distances) of cyt *b*, and *C*-mos among species of the genus *Goniurosaurus* were calculated and summarized by species. The optimal models were selected under the Bayesian Information Criterion (BIC) using PartitionFinder 2.1.1 (Lanfear et al. 2017). Phylogenetic analyses were conducted in PhyloSuite (Zhang et al. 2020) using Maximum Likelihood (ML) and Bayesian Inference (BI) approaches under the selected substitution models (K80 + I for *C*-mos; GTR + G for cyt *b* and 16S rRNA). ML nodal support was assessed with 1,000 bootstrap pseudo-replicates (Felsenstein 1985). For the BI analyses, four independent Markov Chain Monte Carlo (MCMC) runs were performed with random starting trees. Each run consisted of 20 million generations, sampled every 1,000 generations, discarding the first 25% as burn-in.

Results

Morphological measurements of the four collected specimens were obtained using a digital vernier caliper, and the data are summarized in Table 1. Comparative morphometric and scalation data for eight *Goniurosaurus* species of the *G. luii* group are presented in Table 2.

Phylogenetic trees were reconstructed using maximum-likelihood (ML) and Bayesian inference (BI) analyses based on concatenated sequences of three genes: mitochondrial cyt *b* (378 bp), 16S rRNA (440 bp), and nuclear *C*-mos (371 bp), yielding a total aligned length of 1,189 bp and including 24 taxa of the genus *Goniurosaurus*. The ML and BI analyses produced highly congruent topologies; consequently, only the BI tree is presented here (Fig. 1). This tree incorporates both Bayesian posterior probabilities (BPP) and ML bootstrap support values (BS) to illustrate a robust phylogenetic framework for the genus. The analyzed taxa were resolved into four

Table 1. Morphological measurements (in mm) and scalation characters of the type specimens of *Goniurosaurus wuzhengjuni* sp. nov. (Abbreviations defined in Materials and Methods). "*" indicated regenerated tail.

	Holotype GXNU2025101603	**Paratype GXNU2025090812**	**Paratype GXNU2025101601**	**Paratype GXNU2025101602**
Sex	Male	Female	Female	Female
SVL	92.3	109.3	101.0	99.6
TaL	74.8	56.2*	87.1	48.8*
AG	36.6	49.5	46.7	44.5
HL	25.5	28.7	26.8	27.3
HW	17.8	20.8	20.2	19.7
SE	10.6	11.4	10.2	11.0
EE	9.2	11.1	10.2	9.2
SVL/HL	3.62	3.80	3.77	3.65
SVL/AG	2.52	2.21	2.19	2.24
HL/HW	1.43	1.38	1.33	1.42
SE/EE	1.15	1.03	1.00	1.20
SPL	9/9	8/8	9/9	9/9
SBL	10/10	9/9	10/9	9/9
SN	7	7	7	7
IN	1	0	1	1
PostIN	2	2	2	2
PM	4	4	4	2
GP	8	8	8	9
CIL	52/47	49/47	51/49	52/54
MB	106	108	101	105
GST	12	11	12	12
TL	27	26	27	27
DTR	22	21	22	22
LD1	13/13	11/11	13/13	11/11
LD4	19/17	17/17	19/17	19/19
LT1	13/12	13/13	13/12	11/11
LT4	25/23	24/24	26/25	26/26
PP	23	0	0	0
PAT	2/2	2/2	2/2	2/2

principal species groups — *G. kuroiwae*, *G. lichtenfelderi*, *G. luii* and *G. yingdeensis* (Fig. 1) — consistent with the group delineations proposed by Grismer et al. (1994, 1999) and Grismer (2000). The four newly collected specimens formed a well-supported monophyletic clade (BPP 1.00/BS 100) nested within the *G. luii* group (BPP 0.96/BS 98). Within this clade, the closest phylogenetic relative was *G. araneus* Grismer, Viets & Boyle, 1999 (BPP 0.98/BS 92).

The uncorrected pairwise genetic distances for mitochondrial cyt *b* divergence ranged from 8.7% to 22.0% relative to other *Goniurosaurus* species (Suppl. material 2). This level of divergence is indicative of interspecific differentiation, comparable to the uncorrected *p*-distances of 3.4% between *G. hainanensis* Barbour, 1908 and *G. lichtenfelderi* Mocquard, 1897; 5.6% between *G. toyamai* Grismer, Ota & Tanaka, 1994 and *G. sengokui* Honda & Ota, 2017; and 7.5% between *G. zhelongi* Wang, Jin, Li & Grismer, 2014 and *G. yingdeensis* Wang, Yang & Cui, 2010. The new lineage formed a genetically distinct, clustering within the same clade as *G. gezhi* Zhu, He & Li, 2020 and *G. chengzheng* Zhu, Liu, Bai, Román-Palacios, Li & He, 2021, both members of the *G. luii* group.

Systematics

***Goniurosaurus wuzhengjuni* Chen & Chen, sp. nov.**

https://zoobank.org/A18D786E-133C-4B33-B84A-DA5384909591

Figs 2, 3

Type materials. ***Holotype.*** • GXNU2025101603, adult male (Fig. 2A), from Baishou Nature Reserve, Yongfu County, Guilin City, Guangxi Zhuang Autonomous Region, China (25.0636°N, 109.7391°E; elevation 323 m a.s.l.) collected by H.L. Chen on 26 October 2025.

Paratypes. • Three adult females GXNU2025090812 (Fig. 2B), GXNU2025101601 (Fig. 2C) – 02 (Fig. 2D), same data to the holotype.

Diagnosis. *Goniurosaurus wuzhengjuni* sp. nov. can be distinguished from its congeners through a distinct combination of morphological characteristics: (1) SVL 92.3–109.3 mm; (2) 0–1 internasals; (3) 2 gular scales bordering the internasals; (4) 8–9 gular scales bordering the postmentals; (5) 26–27 paravertebral tubercles between limb insertions; (6) 23 precloacal pores in males; (7) 7 nasal scales surrounding the nostril; (8) 9–10 sublabials; (9) 47–54 eyelid fringe scales or ciliaria; (10) 11–12 granular scales surrounding dorsal tubercles; (11) 21–22 dorsal tubercle rows at midbody and (12) 101–108

Table 2. Comparisons of morphometric characters (in mm) and scale counts for eight *Goniurosaurus* species within the *luii* group. Character abbreviations are explained in material and methods (data for *G. araneus* and *G. luii* from Grismer et al. 1999; *G. catbaensis* from Orlov and Darevsky 1999; *G. huuliensis* from Orlov et al. 2008; *G. liboensis* from Wang et al. 2013; *G. kwangsiensis* from Yang and Chan 2015; *G. gezhi* from Zhu et al. 2020a; *G. chengzheng* from Zhu et al. 2021).

Species		SVL	SPL	SBL	CIL	PM	GST	TL	MB	LT4	PP	SE:EE
Goniurosaurus wuzhengjuni **sp. nov.**	Mean	100.57	8.75	9.37	50.12	3.5	11.75	26.75	105	24.87	23	1.09
	SD	6.95	0.46	0.53	—	1	2.53	0.5	2.94	1.13	0	0.1
	Range	92–109	8–10	9–10	47–54	2–4	11–12	26–27	101–108	17–19	23	1.00–1.20
G. chengzheng	Mean	107	8.5	9.5	54.5	3	11.75	29	128	23	20	0.99
	SD	0	0.7	0.7	2.12	0	1.41	0	12.73	0	0	0
	Range	107	8–9	9–10	53–56	3	11–13	29	119–137	23	20	0.99
G. gezhi	Mean	77	9.33	9	48.33	4	11.33	34.67	136.83	23.5	19.33	1.17
	SD	6.64	0.52	0.63	3.26	1.41	0.82	3.78	10.03	1.52	1.15	0.07
	Range	71–84	9–10	8–10	44–52	3–5	10–12	32–39	123–151	21–25	18–20	1.09–1.21
G. araneus	Mean	—	8.8	8.7	64	5.3	9.8	35.8	135.7	23.5	19.8	—
	SD	—	0.98	0.52	2.19	0.82	4.33	2.71	7.26	0.55	1.71	—
	Range	115–124	8–10	8–9	61–67	4–6	10–14	32–38	129–147	23–24	18–22	—
G. luii	Mean	—	9.5	10	59.5	3	12.2	33.8	134.5	23.5	26	—
	SD	—	0.55	0.63	1.87	0.89	1.34	0.75	12	1.38	2.58	—
	Range	107–116	9–12	9–11	57–61	2–4	9–14	33–34	119–144	21–24	23–29	—
G. huuliensis	Mean	115	10.4	9.8	43.5	2.4	12.2	34.6	123.6	17.4	26.75	1.28
	SD	3.69	0.52	0.63	0.95	0.55	0.44	0.89	3.91	0.7	1.26	0
	Range	109–117	10–11	9–11	41–44	2–3	12–13	34–36	118–129	17–19	25–28	1.28
G. kwangsiensis	Mean	104	9.38	8.38	54.5	4	11.5	30.25	125.25	24.12	32	1.31
	SD	4.77	0.84	0.82	1.17	1.41	1.21	2.36	2.75	0.82	1.41	0.03
	Range	98–109	8–10	7–9	52–58	3–6	10–13	27–32	122–128	22–27	31–33	1.28–1.34
G. catbaensis	Mean	—	8.8	7.7	53.7	2.7	9.7	33.3	119.3	23.3	18.7	1.12
	SD	—	0.4	0.8	1	0.6	1.5	0.6	7.5	0.8	2.5	0.07
	Range	85–112	8–9	6–8	52–55	2–3	8–11	33–34	112–127	22–24	16–21	1.03–1.15
G. liboensis	Mean	106	10.38	10.38	55.83	4	12	27.67	128	24.33	23	1.23
	SD	3.1	0.92	0.92	2.64	1.15	1.12	0.58	1.15	1.21	0	0.05
	Range	103–110	9–12	9–12	52–59	3–5	10–13	27–28	127–129	23–26	23	1.20–1.30

Subadults are not included, "—" unavailable data.

midbody scale rows; (13) 2 postcloacal tubercle present on each side; (14) a light yellow dorsal ground coloration on the head, body, and limbs covered with dense, irregular black blotches.

Description. Holotype. GXNU2025101603, adult male; SVL 92.3 mm; TaL 74.8 mm; AG 36.6 mm; SE 10.6 mm; EE 9.2 mm; HW 17.8 mm; HL 25.5 mm; SVL/AG 2.52; SVL/HL 3.62; HL/HW 1.43; SE/EE 1.15.

The head is wider than the neck and dorsally covered with uniform granular scales interspersed with small tubercles. The rostral scale is convex and wider than high, bordered laterally by the first supralabial and prenasal scales, and posteriorly by the supranasal scale. Each external naris is encircled by seven nasal scales—anteriorly by the prenasal, dorsally contacting the supranasal and one granular scale (noted on the right side), and posteriorly by two smaller granular scales (Fig. 3C). There are nine rectangular supralabials on each side (9/9). The eyes are relatively large with vertical pupils. A suborbital skin fold extends posteroventrally across the angle of the jaw. The tympanum is deeply recessed and bordered anteriorly by two spinose scales. The mental scale is bordered laterally by the first infralabials and posteriorly by four postmentals. There are ten rectangular infralabials on each side (10/10).

The neck is narrower than the body. Dorsal body tubercles are each surrounded by 11 or 12 granular scales. There are 21–22 rows of dorsal tubercles at midbody, and 26–27 paravertebral tubercles between limb insertions. The body is relatively slender, bearing 101–108 granular scales around midbody. Larger ventral scales transition abruptly to smaller granular scales just anterior to the vent. There are 23 precloacal pores arranged in a continuous transverse series that does not extend onto the proximal thighs (Fig. 3F). Two enlarged postcloacal tubercles are present laterally at the vent level.

The limbs are long and slender; dorsally they bear granular scales and closely spaced tubercles, while ventrally, the scales are flat, ranging from juxtaposed to subimbricate. The hindlimbs are larger than the forelimbs. The dorsal surfaces of both manus and pes bear granular scales, with the pes bearing several conical tubercles. The ventral surfaces of the limbs are covered with large granular scales. Subdigital lamellae counts are as follows: 13/13 on the first finger, 19/17 on the fourth finger, 13/12 on the first toe, and 25/24 on the fourth toe.

G. wuzhengjuni **sp. nov.**
Guilin, Guangxi, China

G. wuzhengjuni **sp. nov.**
Guilin, Guangxi, China

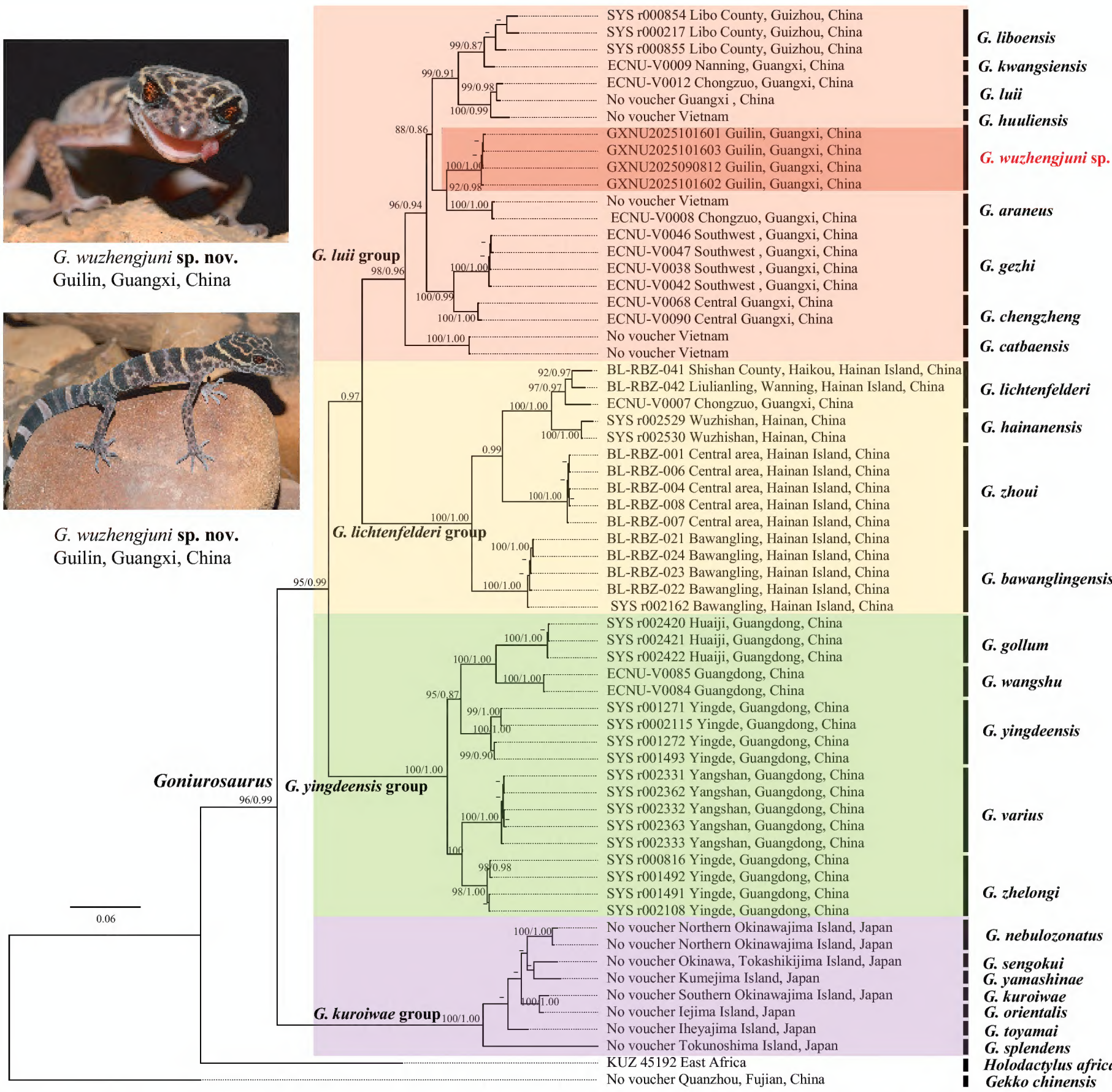

Figure 1. A Bayesian Inference phylogenetic tree of the genus *Goniurosaurus* and two outgroups taxon. Nodal support values are shown above branches as ML bootstraps (BS) and Bayesian posterior probability (BPP). Support values with BPP lower than 0.85 and BS lower than 85 was display as "-".

The original tail is slender at the base, gradually thickening towards the middle, and tapering to a blunt tip, bearing six distinct bands along its length.

Coloration in life. The head, body, and limbs exhibit a grayish-white dorsal ground color with dense, irregular black blotches, some of which are partially fused on the head. The iris is orange. A pale-yellow nuchal loop is present, with a rounded posterior margin. Three pale-yellow bands occur on the body between the limb insertions and a postsacral band is located at the base of the tail. The ventral surfaces of the head, body, and limbs are white. The original tail bears a black ground color with distinct white bands, whereas the regenerated tail shows irregular white markings that coalesce toward its tip.

Comparisons. *Goniurosaurus wuzhengjuni* sp. nov. is assigned to the *G. luii* group by a unique combination of morphological characteristics—more than 16 precloacal pores in males, claws encased in scales, and a slender, splayed body and limbs—consistent with the original definition of the group.

The new species differs from its sister taxon, *G. araneus*, by having fewer eyelid fringe scales (CIL, 47–54 vs. 61–67), fewer scales around midbody (MB, 101–108 vs. 129–147), fewer subdigital lamellae under the fourth toe (LT4, 17–19 vs. 23–24), and more precloacal pores (PP, 23 vs. 18–22).

Additional scalation characters further emphasize the distinctiveness of *G. wuzhengjuni* sp. nov., as shown by the following combination of traits: (1) fewer MB (101–108 in *G. wuzhengjuni* vs. 123–151 in *G. gezhi*, 119–137 in *G. chengzheng*, 119–144 in *G. luii* Grismer, Viets & Boyle, 1999, 118–129 in *G. huuliensis* Orlov, Ryabov, Nguyen, Nguyen & Ho, 2008, 122–128 in *G. kwangsiensis* Yang & Chan, 2015, 112–127 in *G. catbaensis*

Figure 2. Photograph of *Goniurosaurus wuzhengjuni* sp. nov. from Guangxi, China in live. **A.** Adult male (Holotype, GXNU2025101603); **B.** Adult female (Paratype, GXNU2025090812); **C.** Adult female (Paratype, GXNU2025101601); **D.** Adult female (Paratype, GXNU2025101602). (Photos by Zening Chen and Hanzhang Cai).

Ziegler, Truong, Schmitz, Stenke & Rösler, 2008 and 127–129 in *G. liboensis* Wang, Yang & Grismer, 2013); (2) a different number of PP (23 in *G. wuzhengjuni* vs. 18–20 in *G. gezhi*, 20 in *G. chengzheng*, 16–21 in *G. catbaensis* and 25–28 in *G. huuliensis*); (3) fewer LT4 (17–19 in *G. wuzhengjuni* vs. 23 in *G. chengzheng*, 21–24 in *G. luii*, 22–27 in *G. kwangsiensis*, 22–24 in *G. catbaensis* and 23–26 in *G. liboensis*); (4) distinct CIL counts (47–54 in *G. wuzhengjuni* vs. 57–61 in *G. luii* and 41–44 in *G. huuliensis*); and (5) more SBL (9–10 in *G. wuzhengjuni* vs. 6–8 in *G. catbaensis*). Detailed data are summarized in Table 2.

G. wuzhengjuni sp. nov. differs from species of the *G. lichtenfelderi* group by having a more slender body and limbs, a greater number of subdigital lamellae under the first finger (11–13 vs. 6–10), and a broader black band either anterior or posterior to the three pale-yellow body bands. It is distinguished from the *G. kuroiwae* group by the presence of 23 precloacal pores in males (vs. absence in that group) and claws encased by four scales rather than unsheathed. The new species is further separated from the *G. yingdeensis* group by a greater number of precloacal pores.

Variation. Measurements and scalation data for the type series are provided in Table 1. The paratypes generally conform to the holotype in coloration and overall morphological proportions, with the following exceptions: the ratio of snout–vent length to axilla–groin distance (SVL/AG) is 2.52 in the male (n = 1) and 2.19–2.21 in females (n = 3). Paratype GXNU2025090812 differs from the remaining specimens in the following aspects: (1) the absence of an internasal scale, present in the others; (2) 11 granular scales surrounding the dorsal tubercles, compared to 12 in the others; and (3) 26 paravertebral tubercles between limb insertions, rather than 27 as in the others.

Etymology. The specific epithet *wuzhengjuni* honors Professor Zhengjun Wu for his significant contributions to the study of Sauria. His research team pioneered the use of AI-based tail pattern recognition technology, which has greatly advanced the conservation and research of the nationally first-class protected species *Shinisaurus crocodilurus*, thereby supporting population-recovery efforts. The proposed common names are "Wu's Cave Gecko" (in English) and "武氏睑虎" (wǔ shì jiǎn hǔ in Chinese).

Distribution and ecology. *Goniurosaurus wuzhengjuni* sp. nov. was discovered in the karst regions of northern Guangxi, China, at elevations ranging from 280 to 351 meters in areas with dense arborous vegetation (Fig. 4A). The species is nocturnal and was frequently observed on limestone surfaces near roadside slopes or around limestone accumulations at cave entrances (Fig. 4B, C).

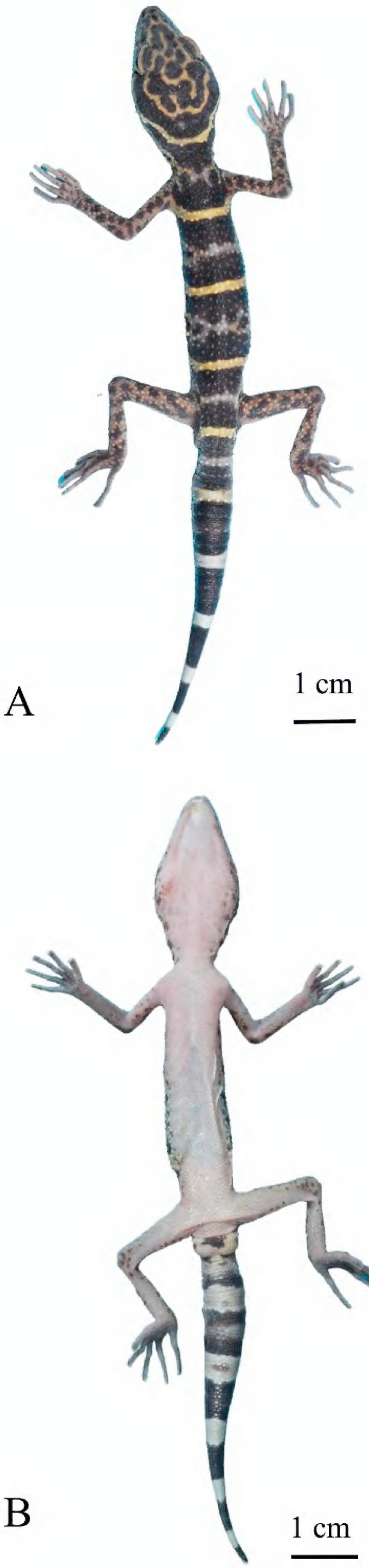

Figure 3. *Goniurosaurus wuzhengjuni* sp. nov. of holotype, GXNU2025101603. **A.** Dorsal view; **B.** Vental view; **C.** Dorsal surface of the head; **D.** Ventral surface of the head; **E.** Precloacal region. (Photos by Huiling Chen).

Figure 4. Habitat of *Goniurosaurus wuzhengjuni* sp. nov. at the type locality. **A.** Inhabited environment; **B, C.** Microhabitat where they were discovered. (Photos by Huiling Chen).

Discussion

Although most *Goniurosaurus* species show a distinct preference for karst habitats, some members of the *G. kuroiwae* and *G. lichtenfelderi* groups are not strictly confined to limestone environments (Wang et al. 2014; Liang et al. 2018; Qi et al. 2020a, 2020b, 2025; Grismer et al. 2021). This pattern may be explained by the absence of competitors or predators in insular habitats, which likely expanded the fundamental ecological niche of their ancestors and allowed certain species to occupy a wider range of habitat (Grismer et al. 2021).

Karst ecosystems not only provide habitats with relatively stable microclimatic conditions but also serve as crucial refugia for relict lineages (Grismer et al. 2016a; Wood et al. 2017). The discovery of *G. wuzhengjuni* sp. nov. in the Guilin karst region—an area renowned for geomorphological and biotic evolution studies—fills a notable distributional gap within the genus and underscores the potential existence of cryptic endemic taxa in this biodiversity hotspot. This finding highlights the importance of comprehensive biodiversity surveys in karst regions to better understand species diversity and evolutionary history.

Nevertheless, karst habitats are increasingly threatened by fragmentation resulting from land reclamation and urban expansion, leading to a decline in forest cover and the loss of essential microhabitats for *Goniurosaurus* species (Jiang et al. 2014; Grismer et al. 2016a, 2016b). Moreover, the popularity of *Goniurosaurus* in the pet trade—driven by their vivid coloration and distinctive appearance—has led to extensive illegal collection and trade, further exacerbating pressures on wild populations in China. The discovery of the new species thus not only enriches our taxonomic knowledge but also underscores the urgent need for integrated conservation strategies. Such strategies should encompass habitat protection, strict law enforcement, and public education to mitigate threats and preserve karst-adapted species diversity of karst-adapted species.

Guangxi Zhuang Autonomous Region, where *G. wuzhengjuni* sp. nov. was discovered, harbors eight *Goniurosaurus* species, accounting for nearly one-third of the genus's known diversity. This high species richness within a karst-dominated landscape emphasizes the role of karst ecosystems as centers of endemism and evolutionary diversification in *Goniurosaurus*. The description of *G. wuzhengjuni* sp. nov. makes a valuable contribution to our understanding of the adaptive radiation and biogeographical patterns within the genus, further demonstrating the evolutionary significance of these specialized habitats.

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Supplementary material 1

Species and GenBank accession numbers used in this study

Authors: Hui-Ling Chen, Jia-Yi Yu, You-Bang Li, Yu-Hui Li, Ze-Ning Chen

Data type: xlsx

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Link: https://doi.org/10.3897/zse.102.177343.suppl1

Supplementary material 2

Uncorrected distance(%) between Goniurosaurus species based on the 378 bp sequences of cyt b gene

Authors: Hui-Ling Chen, Jia-Yi Yu, You-Bang Li, Yu-Hui Li, Ze-Ning Chen

Data type: xlsx

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